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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 00:14:43 ; Search time 368.413 Seconds

(without alignments)
10012.591 Million cell updates/sec

Title: US-09-001-737-7_COPY_15_1652

Sequence: 1 ATGCCAAGAAATCAATTT.....TGGGTGGATGGCGGATAA 1638

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
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19: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description
1	1638	100.0	1661	AAH86155
2	1620.2	98.9	1635	ABH69160
3	1413.4	86.3	2683	AAH56861
4	1140.4	69.6	1306	AAH56862
5	1122.6	68.5	1305	AAH56865
6	1062.4	64.9	1620	ABH69159
7	1062.4	64.9	2155561	ABH71527
8	1039.2	63.4	1623	AAH90800
9	1038.4	63.4	1926	AAH25036

10	1038	63.4	1654	AAH86153
11	1036	63.2	1647	AAH90806
12	1036	63.2	2107	AAH56860
13	1034.4	63.2	5365	AAV52210
14	1029.6	62.9	2401	AAH56859
15	954.2	58.3	2365589	ABA90521
16	942.6	57.5	3625	AAH56859
17	831.2	50.7	1901	AAH70705
18	823.2	50.3	213251	AAH56868
19	785.4	47.9	1957	AAH56867
20	772	47.1	1958	AAH56867
21	760.6	46.4	1570	AAH56867
22	755.4	46.1	1620	AAH56868
23	755.4	46.1	3885	AAH56868
24	723.4	44.8	1623	AAH56865
25	721.4	44.0	2712	AAH56865
26	704.2	43.0	1647	AAH56865
27	704.2	43.0	4972	AAH56865
28	654.2	39.9	96109	AAH56865
29	615.8	37.6	640681	AAH56864
30	608.2	37.1	613	AAH56864
31	604.2	36.9	609	AAH56863
32	589.8	36.0	1647	AAH48498
33	589.8	36.0	1647	AAH48498
34	589.8	36.0	1647	AAH48498
35	589.8	36.0	1741	AAH56858
36	589.8	36.0	2155	AAH56858
37	589.8	36.0	4524	AAH56858
38	587.6	35.9	1665	AAH56858
39	583.4	35.6	2032	AAH56857
40	577.2	35.2	2066	AAH56857
41	565.2	34.5	1652	AAH56857
42	552.8	33.7	1635	AAH56857
43	550	33.6	2465	AAH56857
44	549.8	33.6	910715	AAH56857
45	536.8	32.8	1635	AAH56857

ALIGNMENTS

RESULT 1
ID: AAH86155 standard. DNA: 1661 BP.
AC: AAH86155:
XX 22-SEP-1999 (first entry)
XX
XX
DE DNA encoding a Streptococcus pyogenes heat shock protein (Hsp)60-2.
KM Heat shock protein: Hsp60-2; Immune response; immunological carrier;
KW cancer control; tumour; sarcoma; cancer; gene therapy; ss.
XX
XX Streptococcus pyogenes.
OS
XX
XX
PN MO9935270-A1.
XX
XX 15-JUL-1999.
PD
XX
XX 29-DEC-1998; 98MO-CA01203.
XX
XX 31-DEC-1997; 97US-0001737.
PR
XX
XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
PA
XX
XX Mizen L, Wisniewski J;
PI WPI: 1999-430397/36.
XX
XX P-PSDB: AAV23904.
XX
XX New nucleic acid encoding heat shock protein-60 from Streptococcus,
PT useful in vaccines, as carriers for other immunogens, as anticancer

PT agents and for diagnosis
XX
PS Claim 3; Flg 4A-B; 176pp; English.
XX

cc The present sequence encodes a heat shock protein, designated Hsp60-2
cc The protein, its fragments, variants and fusion proteins are

used to elicit or enhance an immune response against *Streptococcus*, and to elicit a similar response to a target antigen fused to the protein. Unlike other immunological carriers, Hsp60 proteins are not immunosuppressive so provide an increased response to any conjugated fused antigen. Also, where used for cancer control, they lack the side effects associated with endotoxins. They can also be used to detect specific antibodies and in treatment or prevention of tumours (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or liver). The Hsp60 polynucleotide is used for recombinant production of the protein, as a source of primers and probes for detecting streptococci in standard hybridization/amplification assays, and therapeutically in gene therapy vectors.

50 Sequence 1661 BP; 512 A; 308 C; 407 G; 434 T; 0 other;

Query match	100.0%;	Score 1638;	DB 20;	Length 1661;
Best local similarity	100.0%;	Pred. No. 0;		

Matches 1638; Conservative 0; Mismatches

Matches 1638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	721	ACCAACCCCTCATTACTCACTTTTGGACAGATGAGTAAAGTGTGAAGACCTTCAACCTT	780
Db	735	ACCAACCCCTCATTACTCACTTTTGGACAGATGAGTAAAGTGTGAAGACCTTCAACCTT	794
QY	781	GCTTCGAACAAGATTGTAAGTACTTTAAATGAGTGTGCTGCAAAAGCCACAGATTGGT	840
Db	795	GCTTCGAACAAGATTGTAAGTACTTTAAATGAGTGTGCTGCAAAAGCCACAGATTGGT	854
QY	841	GATCCCTCCTAAACCTATGCTTGAAGACATTCGATCTTGAAGTGTGACATGATTACA	900
Db	855	GATCCCTCCTAAACCTATGCTTGAAGACATTCGATCTTGAAGTGTGACATGATTACA	914
QY	901	GAGGATCTAGAGCTTAATTTAAAGATGCTACAAATGACAGCCCTGTGAAGAGGCTGTAG	960
Db	915	GAGGATCTAGAGCTTAATTTAAAGATGCTACAAATGACAGCCCTGTGAAGAGGCTGTAG	974
QY	961	ATTACAGTATTAAGATAGCACAGTAAATGTTGAAGATTAGAGAGTTCACAGACTATT	1024
Db	975	ATTACAGTATTAAGATAGCACAGTAAATGTTGAAGATTAGAGAGTTCACAGACTATT	1038

[illegible]

DB 1035 GCCTACCGGATTTGCACTGATTAAATCGCAATTAGAAACACACACTTCTGACTTTGACCGT 109

QY 1081 GAAAACTACAGAAGCTTTGGCGAATTAGCTGGTGTAGCTGTTATCAAGTAGGA 1144

Db 1095 GAAAACTACAAGAACGTTGGCGAAATTAGCTGGTGTAGCTTTATCAAGTAGGA 115

QY 1141 GCTCCACAGAGACAGCTTTAAAGAATGAACTTCGCATTGAGGATGCTCTAAATGCT 1200

Pb 1155 GCTCCACAGAGACACGCTTTTAAADACDAAATGCAAACTTTCCCAATGACACGCAATGACCTCTTAAATTCCT 1214

Year	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

1201 ACACGTGCAGCCGTTGAAGAGAGGTATCGTTGCTGCTGCTGCTGCAACAGCAGCACTATTACGGTT 1260

Db 1215 ACACGTCAGCCGTTGAGAGGATATCGTTGCTGCTGGTGGTGAACAGCACTTATTACGGTT 1274

OY 1261 ATTGAAAAAGTAGCAGCTCTTGAGCTTGAGGGCGATGATGCTACTGAGCTAACATTTCG 1320

Db 1275 ATGAAAAGTAGCAGCTTGAAGCTTGAGGGCGATGATGCTACTGAGCGTAACATTGTG 1334

[illegible][illegible]

Db 1335 CTTGCTGCTCAGAGAGCCTGTACGTCAATTGCTTTAATGCTGGGTACGAGAGGCTCC 1390

QY 1381 GTAGTTATTGACCACTTGAAAACAGCCCTGCAGGACAGGATTTAATGCTGCAACAGGT 1440

Db 1395 GTAGTTATGACAAGTTGAANAACAGCCCTGCAGGACAGATTTAATGCTGCACACAGGT 1454

1441 GAGTGGGTGATATGATTAAACAGGAAATCATTTGACCCCTGTCAAAGTAAACAGAAATCAGCG 1500

[illegible]

CC 1409 CAGGATGATTTTAAACAGGAATCATTGACCCTGTCAAGGTACACAGATCAGCG 1518

1501 CTTCAAAATGCAGCTTCTGTAGCTAGTCTTATTTTGGACACACAGAGACAGTTGTTGCTAAT 1560

Db 1515 CTTCAAAATGCAGCTTCTGTAGCTAGTCTTATTTTGACACAGAGCAGTTGTTGCTAAT 1574

QY 1561 AAACCTGAACGAGCTACGCCAGCGCCAGCAATGCCAGCAGGTATGGATCCAGGATGATG 1620

Db 1575 AACCTGACCAAGCTACGCCAGGCCAGCAATGCCAGCAGTTATGGATCCAGGAATGATG 1634

[illegible]

0507 WWWWCCCCCCCCCCCCCC
1701 CCCCCCCCCCCCCCCC

Db . 1635 GGTGGGATGGCCGATAA 1652

SECTION 2

RESOL 2
ABN69160

ID ABN69160 standard; DNA; 1635 BP.
XX

AC ABN69160;

DT	01-JUL-2002 (first entry)
AA	

XX

DE Streptococcus polynucleotide SEQ ID NO 6233.
 XX Streptococcus: GAS: GBS: group B streptococcus: Streptococcus agalactiae:
 KM group A streptococcus: Streptococcus pyogenes: antibacterial: gene:
 KM antiinflammatory: infection: vaccine: meningitis: gene therapy: ds.
 OS Streptococcus pyogenes.
 PN WO200234771-A2.
 PD 02-MAY-2002.
 PF 29-OCT-2001: 2001WO-GB04789.
 PR 27-OCT-2000: 2000GB-0026333.
 PR 24-NOV-2000: 2000GB-0028727.
 PR 07-MAR-2001: 2001GB-0005640.
 PA (CHIR-) CHIRON SPA.
 XX (GENO-) INST GENOMIC RES.
 PI Telford J, Maignani V, Margalit Ros YI, Grandi G, Fraser C:
 PI Tefellin H;
 DR WPI: 2002-352536/38.
 DR P-PSDB: ABP28529.
 XX New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PT for detecting a compound that binds to the protein -
 PS Claim 7: Page 3785-3786: 4525pp: English.
 XX The invention relates to a protein (ABP25413-ABP30895) from group B
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (1), nucleic acids encoding (1), ABN6044-ABN71526 and
 CC antibodies that bind (1) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (1) are used to detect Streptococcus in a
 CC biological sample. (1) is used to determine whether a compound binds to
 CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (1) may be used to recombinantly produce (1) and may be
 CC used in gene therapy. Antibodies to (1) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.
 XX Sequence 1635 BP: 504 A: 303 C: 397 G: 431 T: 0 other:
 SQ
 Query Match 98.9%; Score 1620.2; DB 24; Length 1635;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1622: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 241 AATGATATGCTGTGATAGGACGACTACTGCAACAGTTTGGACACAGCCATTGTCAT 300
 DB 247 AATGATATGCTGTGATAGGACGACTACTGCAACAGTTTGGACACAGCCATTGTCAT 306
 QY 301 GAAGACATTAATAATGTGACACAGGTGCTAATCCAAATTTGGTATCCGTGAGGATGAA 360
 DB 307 GAAGACATTAATAATGTGACACAGGTGCTAATCCAAATTTGGTATCCGTGAGGATGAA 366
 QY 361 ACAGCAACGACACAGCTTGTGAAGCCTTGAAGCCATTGCTCAACCTGTATCTGGCAG 420
 DB 367 ACAGCAACGACACAGCTTGTGAAGCCTTGAAGCCATTGCTCAACCTGTATCTGGCAG 426
 QY 421 GAAGCTATGCTCAGGTGCTGAGTATCATCAGCTCTGAAAAGTTGAGAGATATATC 480
 DB 427 GAAGCTATGCTCAGGTGCTGAGTATCATCAGCTCTGAAAAGTTGAGAGATATATC 486
 QY 481 TCAGAGATGAGAGCGTGTGGCAGACAGATGTTGATTACATCCGAATATCTGAGGT 540
 DB 487 TCAGAGATGAGAGCGTGTGGCAGACAGATGTTGATTACATCCGAATATCTGAGGT 546
 QY 541 ATGGAACAGACATTAAGTGTGAAGCAGTCAATTTGACCGTGTACCTGTCTCAA 600
 DB 547 ATGGAACAGACATTAAGTGTGAAGCAGTCAATTTGACCGTGTACCTGTCTCAA 606
 QY 601 TACATGTGACAGACATGAAAAAATGTTGACAGCTTGAATAAACCATTATCTATATC 660
 DB 607 TACATGTGACAGACATGAAAAAATGTTGACAGCTTGAATAAACCATTATCTATATC 666
 QY 661 ACAGATTAATAATGTGCAACATCCAGACATTTGCCACTGATGAGAGATCTTAA 720
 DB 667 ACAGATTAATAATGTGCAACATCCAGACATTTGCCACTGATGAGAGATCTTAA 726
 QY 721 ACCAAGCTCATTAATCTATTATGAGATGATGATGATGATGATGATGATGATGATGATGAT 780
 DB 727 ACCAAGCTCATTAATCTATTATGAGATGATGATGATGATGATGATGATGATGATGATGAT 786
 QY 781 GCTTGAACAAAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 840
 DB 787 GCTTGAACAAAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 846
 QY 841 GATGCTGTAAGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 900
 DB 847 GATGCTGTAAGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 906
 QY 901 GAGATCTAGAGCTTGAATTAAGATGCTACATGACAGCCTTGGACAGGCTGCTAAG 960
 DB 907 GAGATCTAGAGCTTGAATTAAGATGCTACATGACAGCCTTGGACAGGCTGCTAAG 966
 QY 961 ATTACAGTTGTAAGATAGCAGATGATTTGTTGAAGTTGAGAGTTGAGAGCTAAT 1020
 DB 967 ATTACAGTTGTAAGATAGCAGATGATTTGTTGAAGTTGAGAGTTGAGAGCTAAT 1026
 QY 1021 GCTAACGCTATGCTACTGATTAATGCAATTAGAAACACACTTGTGATGACCT 1080
 DB 1027 GCTAACGCTATGCTACTGATTAATGCAATTAGAAACACACTTGTGATGACCT 1086
 QY 1081 GAAATACATCAAGACGTTTGGGAAATTAAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1140
 DB 1087 GAAATACATCAAGACGTTTGGGAAATTAAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1146
 QY 1141 GCTCAACAGACAGCTTAAAGAAATGAATGAACTTGCATGAGATGCTCTAAATGCT 1200
 DB 1147 GCTCAACAGACAGCTTAAAGAAATGAATGAACTTGCATGAGATGCTCTAAATGCT 1206
 QY 1201 ACAGCTGAGCGCTTAAGAGATGATGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1260
 DB 1207 ACAGCTGAGCGCTTAAGAGATGATGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1266
 QY 1261 ATTGAATAAGTACAGCTTGTGAGTGTGAGGCGATGATGCTACTGAGAGTAACTGTG 1320
 DB 1267 ATTGAATAAGTACAGCTTGTGAGTGTGAGGCGATGATGCTACTGAGAGTAACTGTG 1326
 QY 1321 CTTCGTCTGTAAGAGCGCTGTACGTCAAAATTTGCTTAAATGCTGAGTACAGAGCTCTC 1380

DB 1327 CTTGCTGCTCTAGAGAGCCTGACCTAAATGCTTTAAAGCTGGGTACGAGGCTCC 1386
 OY 1361 GTAGATTATGACAGATTGAAAAAAGCCCTCCAGAGACGATTAAATGCTCAACAGGT 1440
 DB 1367 GTAGATTATGACAGATTGAAAAAAGCCCTCCAGAGACGATTAAATGCTCAACAGGT 1446
 OY 1441 GAGTGGCTGATGATGATTAACAGAAATCATGACCTGCTCAAGTAACAGATCAGC 1500
 DB 1447 GAGTGGCTGATGATGATTAACAGAAATCATGACCTGCTCAAGTAACAGATCAGC 1506
 OY 1501 CTTCAAAATGACGCTCTGCTAGCTGCTTATTTTGCACAGAGAGATGCTGCTAAT 1560
 DB 1507 CTTCAAAATGACGCTCTGCTAGCTGCTTATTTTGCACAGAGATGCTGCTAAT 1566
 OY 1561 AAACGTGAACGAGCTAGCGAGCGCCAGCAATCCGACAGATGATGATCCAGAAATGATG 1620
 DB 1567 AAACGTGAACGAGCTAGCGAGCGCCAGCAATCCGACAGATGATGATCCAGAAATGATG 1626
 OY 1621 GCTGG 1625
 DB 1627 GCTGG 1631

RESULT 3

AAH56861
 ID AAH56861 standard; DNA; 2683 BP.

AAH56861;
 06-SEP-2001 (first entry)

DE 5. pyogenes groEL gene partial sequence SEQ ID NO:7.

XX Antisense oligonucleotide; groEL; groEL; inhibitor; growth;
 XX microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;
 XX Streptococcus pyogenes; Streptococcus aureus; Pseudomonas aeruginosa;
 XX antibacterial; antiviral; antiproliferative; antisense therapy;
 XX microbial infection; ds.

XX Streptococcus pyogenes.

XX NO200136625-A2.

XX 25-MAY-2001.

XX 20-NOV-2000; 2000MO-CA01347.

XX 18-NOV-1999; 99US-0166249.

XX (GENE-) GENESENSE TECHNOLOGIES INC.

XX Wright JA, Young AH, Dugourd D;

XX WPI; 2001-355633/37.

XX Novel antisense compounds targeting nucleic acid encoding groEL or
 PT groEL gene of microorganism, which hybridize with and inhibit
 PT expression of the genes, useful to inhibit growth of microorganism
 PT having the genes.

XX Disclosure: Fig 7; 110pp; English.

XX The present invention specifically claims AAH56368 to AAH56832 which are
 CC antisense oligonucleotides to nucleotide sequences encoding groE. More
 CC generally, antisense compounds (I) comprising antisense oligonucleotides
 CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat
 CC shock protein (HSP)60) (G), and groES (HSP10) (G) gene from a
 CC microorganism, where the antisense compound is complementary to G, or
 CC G of a microorganism and specifically hybridizes with and inhibits the
 CC expression of G, or G, is claimed. (I) have antibacterial, antiviral
 CC and antiproliferative activities, and can be used in antisense therapy
 CC and for inhibition of expression of groES or groEL. (I) are useful for

CC Inhibiting expression of G, or G, in cells or tissues in vitro. (I) are
 CC also useful for inhibiting the growth of a microorganism, or inhibiting
 CC the expression of G, or G, gene in a microorganism (a bacterial cell or
 CC a virus) having a G, or G, gene which involves administering to the
 CC microorganism or to a cell infected with the microorganism, (I). (I) are
 CC also useful for treating a mammalian pathological condition mediated by
 CC the microorganism which involves identifying a eukaryotic organism
 CC or G, gene and administering (I) such that the growth of microorganism
 CC is inhibited. The antisense compounds are utilized for diagnostics,
 CC therapeutics, prophylaxis and as research reagents and kits, e.g., to
 CC prevent or delay microbial infections in humans. They are also useful as
 CC molecular weight markers. AAH56368 to AAH56367 and AAH56832 to AAH56854
 CC represent PCR primers for groE sequences which are used in the
 CC exemplification of the present invention. AAH56855 to AAH56870 represent
 CC groE nucleotide sequence given in the present invention.

XX Sequence 2683 BP; 808 A; 490 C; 593 G; 792 T; 0 other;

Query Match 86.3%; Score 1413.4; DB 22; Length 2683;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 1423; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 187 GATCATTTTGAAGAAATGAGGAGCAAAATGCTGCTGAGAGCTGCTTAAACCAATGAT 246
 DB 1 GATCATTTTGAAGAAATGAGGAGCAAAATGCTGCTGAGAGCTGCTTAAACCAATGAT 60
 OY 247 ATTGCTGTGATGAGGAGCACTACTGCAACAGTTTGTGACCAAGCCATTGCTCATAGGA 306
 DB 61 ATTGCTGTGATGAGGAGCACTACTGCAACAGTTTGTGACCAAGCCATTGCTCATAGGA 120
 OY 307 CTTAAAAATGTGACAGCAGGTGCTAATCCAAATGATGCTGAGAGCATGTAACAGCA 366
 DB 121 CTTAAAAATGTGACAGCAGGTGCTAATCCAAATGATGCTGAGAGCATGTAACAGCA 180
 OY 367 ACAGCAACAGCTGTTGAAGCCTTGAAGCCATTGCTCAACCTGATGCTGCAAGAACT 426
 DB 181 ACAGCAACAGCTGTTGAAGCCTTGAAGCCATTGCTCAACCTGATGCTGCAAGAACT 240
 OY 427 ATTGCTGTGATGAGGAGCACTACTGCAACAGTTTGTGACCAAGCCATTGCTCATAGGA 486
 DB 241 ATTGCTGTGATGAGGAGCACTACTGCAACAGTTTGTGACCAAGCCATTGCTCATAGGA 300
 OY 487 GCTATGAGAGCTGTGAGGAGCAAGATGCTGATACCATGGAAGATGCTGAGATGGA 546
 DB 301 GCTATGAGAGCTGTGAGGAGCAAGATGCTGATACCATGGAAGATGCTGAGATGGA 360
 OY 547 ACAGCACTGAAGCTGTTGAAGCCTTGAAGCCATTGCTCAACCTGATGCTGCAAGAACT 606
 DB 361 ACAGCACTGAAGCTGTTGAAGCCTTGAAGCCATTGCTCAACCTGATGCTGCAAGAACT 420
 OY 607 GTCACAGCAATGAAAAATGCTGACAGCCTGGAAGCCATTATCTTAATCAACGAT 666
 DB 421 GTCACAGCAATGAAAAATGCTGACAGCCTGGAAGCCATTATCTTAATCTTAATCAACGAT 480
 OY 667 AAAAAAGTCAAAACATCAAGCAATTTTGCACCTAGTGAAGAGTTTAAACCAAC 726
 DB 481 AAAAAAGTCAAAACATCAAGCAATTTTGCACCTAGTGAAGAGTTTAAACCAAC 540
 OY 727 CGTCCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 786
 DB 541 CGTCCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 OY 787 AACCAATTCGCTGATCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 846
 DB 601 AACCAATTCGCTGATCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 OY 847 CGTAAAGCTATGCTTGAAGCAATTTCTTATCTTACAGGTGCTACAGTATCAAGAGAT 906
 DB 661 CGTAAAGCTATGCTTGAAGCAATTTCTTATCTTACAGGTGCTACAGTATCAAGAGAT 720
 OY 907 CTAGAGCTTGAATTAAGATGCTCAATGACAGCCTTGGACAGCTCTCAAGATTACA 966

XX	PA	(GENE-) GENSENSE TECHNOLOGIES INC.
XX	PI	Wright JA, Young AH, Dugourd D;
XX	DR	WPI: 2001-355633/37.
XX	PT	Novel antisense compounds targeting nucleic acid encoding groEL or
PT	PT	groS gene of microorganism, which hybridize with and inhibit
PT	PT	expression of the genes, useful to inhibit growth of microorganism
PT	PT	having the genes -
PS	PS	Disclosure: Fig 8; 110pp: English.
XX	XX	
CC	CC	The present invention specifically claims AAH56368 to AAH56833 which are
CC	CC	antisense oligonucleotides to nucleotide sequences encoding groE. More
CC	CC	generally, antisense compounds (I) comprising antisense oligonucleotides
CC	CC	of 3-50 bases targeted to a nucleotide sequence encoding groE (heat
CC	CC	shock protein (HSP60) (GL) and groES (HSP10) (GS) gene from a
CC	CC	microorganism, where the antisense compound is complementary to GL or
CC	CC	GS of a microorganism and specifically hybridizes with and inhibits the
CC	CC	expression of GL or GS, is claimed. (I) have antibacterial, antiviral
CC	CC	and antiproliferative activities, and can be used in antisense therapy
CC	CC	and for inhibition of expression of groES or groEL. (I) are useful for
CC	CC	inhibiting expression of GL or GS in cells or tissues in vitro. (I) are
CC	CC	also useful for inhibiting the growth of a microorganism, or inhibiting
CC	CC	the expression of GL or GS gene in a microorganism (a bacterial cell or
CC	CC	a virus) having a GL or GS gene which involves administering to the
CC	CC	microorganism or to a cell infected with the microorganism. (I) (I) are
CC	CC	also useful for treating a mammalian pathological condition mediated by
CC	CC	the microorganisms which involves identifying a eukaryotic organism GL
CC	CC	or GS gene and administering (I) such that the growth of microorganism
CC	CC	is inhibited. The antisense compounds are utilised for diagnostics, GL
CC	CC	therapeutics, prophylaxis and as research reagents and kits, e.g., to
CC	CC	prevent or delay microbial infections in humans. They can also be used as
CC	CC	molecular weight markers. AAH56367 to AAH56367 and AAH56833 to AAH56834
CC	CC	represent PCR primers for groE sequences which can be used in the
CC	CC	amplification of the present invention. AAH56855 to AAH56870 represent
CC	CC	groE nucleotide sequence given in the present invention.
XX	XX	
50	50	Sequence 1306 BP: 407 A; 235 C; 308 G; 356 T; 0 other:
		Query Match 59.6%; Score 1140.4; DB 22; Length 1306;
		Best local Similarity 99.9%; P-vec No. 1.9e-286;
		Matches 1141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	484	GAGCTATGAGCGGTGTGGCAACGATGGTGTGATTACCATGAAGAAATCTCGAGTATG 543
DB	2	GAGGTATGAGGCGTGTGGCAACGATGGTGTGATTACCATGAAGAAATCTCGAGTATG 61
QY	544	GAACAGACTGGAAGTGGTGAAGCATGCAATTTGACCGTGGTATCTGTCATAAC 603
DB	62	GAACAGAACTTGAAGTGGTGAAGCATGCAATTTGACCGTGGTATCTGTCATAAC 121
QY	604	ATGCTCAGACAGATGAAAAAATGGTGCACACCTTGAAACCCTTATCTATATACG 663
DB	122	ATGCTCAGACAGATGAAAAAATGGTGCACACCTTGAAACCCTTATCTATATACG 161
QY	664	GATGAAAAAGTGTCAACATCCAAAGCATTTGGCACTCTCTGAGAGAGTCTTAAAC 723
DB	182	GATGAAAAAGTGTCAACATCCAAAGCATTTGGCACTCTCTGAGAGAGTCTTAAAC 241
QY	724	AACCGTCATATTCATTTATGAGATGATGATGATGATGATGATGATGATGATGATG 783
DB	242	AACCGTCATATTCATTTATGAGATGATGATGATGATGATGATGATGATGATGATG 301
QY	784	TTGAAACAATTCGGGTACTTTCAATGTTGGTGCATCAAGGCCAGAGATTGGTGA 843
DB	302	TTGAAACAATTCGGGTACTTTCAATGTTGGTGCATCAAGGCCAGAGATTGGTGA 361
QY	844	CGGTGAAAGCTATGCTTGAACATCTTGATCTTGAACAGTGTGACAGTATTTACAG 903
DB	362	CGGTGAAAGCTATGCTTGAACATCTTGATCTTGAACAGTGTGACAGTATTTACAG 421

Oy	904	GACCTGAGACTGGTAATTAATAAATCTCAAAATGACAGCCCTTGGACAGCGTCGTACAGATT	963
Dd	422	GATCTGAGACTGTGAATTAATAAATCTCAAAATGACAGCCCTTGGACAGCGTCGTACAGATT	481
Oy	964	ACAGTGATTAAGAATGACACAGCTAATTTGTTGAAGGTTGAGGAAGTTCAAGACATTTGGCT	1023
Dd	482	ACAGTGATTAAGAATGACACAGCTAATTTGTTGAAGGTTGAGGAAGTTCAAGACATTTGGCT	541
Oy	1024	AACCGATTGTCACGTGATTAATTCGCATTAATGAAAACMACACTCTCAGTTGACCGTGAA	1083
Dd	542	AACCGATTGTCACGTGATTAATTCGCATTAATGAAAACMACACTCTCAGTTGACCGTGAA	601
Oy	1084	AAACTPACAAGAGCTTTGGCGCAATTTAGCTGGTGGTGTAGCTGTTATCCAAGTAGAGCT	1143
Dd	602	AAACTPACAAGAGCTTTGGCGCAATTTAGCTGGTGGTGTAGCTGTTATCCAAGTAGAGCT	661
Oy	1144	CCACAGAGAGACAGCTTTAAAGAAATTAACCTTCCCATGAGATGCTCTTAATAGCTTACA	1203
Dd	662	CCACAGAGAGACAGCTTTAAAGAAATTAACCTTCCCATGAGATGCTCTTAATAGCTTACA	721
Oy	1204	CGAGACAGCCGTTGAAAGAGTATGCTGGTGGTGGTGGTGAACAGCATTAATAGCGTTATT	1263
Dd	722	CGAGACAGCCGTTGAAAGAGTATGCTGGTGGTGGTGGTGAACAGCATTAATAGCGTTATT	781
Oy	1264	GAAAAAGTAGACGCTCTTGACGTTGAGGCCATATGCTACTGAGACGTACACATTTGTGCTT	1323
Dd	782	GAAAAAGTAGACGCTCTTGACGTTGAGGCCATATGCTACTGAGACGTACACATTTGTGCTT	841
Oy	1324	CCTGCTCTAGAACAGCTGTGACGTCAAAATTTGCTTTAAATCTGGTAGAAGGCTCCGTA	1383
Dd	842	CCTGCTCTAGAACAGCTGTGACGTCAAAATTTGCTTTAAATCTGGTAGAAGGCTCCGTA	901
Oy	1384	GTTATTGACAAAGTTGAAAAGACGCCCTGCGAGAACAGAGATTATTAATGTCACAAAGSTGAG	1443
Dd	902	GTTATTGACAAAGTTGAAAAGACGCCCTGCGAGAACAGAGATTATTAATGTCACAAAGSTGAG	961
Oy	1444	TGGGTGATATGATTTAAACAGATCATTTGACCCTGTCAAAGTAAACAGATAGCGCTT	1503
Dd	962	TGGGTGATATGATTTAAACAGATCATTTGACCCTGTCAAAGTAAACAGATAGCGCTT	1021
Oy	1504	CAAAATGACACTCTGTGATGATCTTATTTTGACACAGAGAGCGTGTCTTAATAA	1563
Dd	1022	CAAAATGACACTCTGTGATGATCTTATTTTGACACAGAGAGCGTGTCTTAATAA	1081
Oy	1564	CCTGACACACTACGCCAGCGCCACAGCAATGCCAGCAGTATGATATCCAGAAATGATGGCT	1623
Dd	1082	CCTGACACACTACGCCAGCGCCACAGCAATGCCAGCAGTATGATATCCAGAAATGATGGGC	1141
Oy	1624	GG 1625	
Dd	1142	GG 1143	
RESULT 5			
ID	AAH56865	standard; DNA; 1305 bp.	
AC	AAH56865;		
XX	06-SEP-2001	(first entry)	
DE	Antibiotic resistant S. pyogenes groEL gene partial sequence SEQ ID:11		
KM	antisense oligonucleotide; groE; groEL; groES; inhibitor; growth;		
KM	microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;		
KM	Streptococcus pyogenes; staphylococcus aureus; pseudomonas aeruginosa;		
KX	antibacterial; antiviral; antiproliferative; antisense therapy;		
KX	microbial infection; ds.		
OS	Streptococcus pyogenes.		
XN	MO200136625-A2.		

[illegible]

OY 361 ACAGCAACAGACAGCTGTGAAAGCTTGAAGCCATGCTCAACCTGATCGCAAG 420
 DB 361 ACAGCTTTTCACAGCAGCTGTGAAAGCTTGAAGCCATGCTCAACCTGATCGCAAG 420
 OY 421 GAAGCTATTCCTCAGCTGTGCAAGATATCAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 480
 DB 421 GAAGCTATTCCTCAGCTGTGCAAGATATCAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 480
 OY 481 TCAGAACTATGAGAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 540
 DB 481 TCAGAACTATGAGAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 540
 OY 541 ATGGAACAGAACTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 600
 DB 541 ATGGAACAGAACTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 600
 OY 601 TACATGCTCAGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 660
 DB 601 TACATGCTCAGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 660
 OY 661 ACGATATTAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 720
 DB 661 ACGATATTAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 720
 OY 721 ACAGAACTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 780
 DB 721 ACAGAACTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 780
 OY 781 GCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 840
 DB 781 GCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 840
 OY 841 GATGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 900
 DB 841 GATGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 900
 OY 901 GAGATCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 960
 DB 901 GAGATCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 960
 OY 961 ATTACAGTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 1020
 DB 961 ATTACAGTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 1020
 OY 1021 GCTACAGTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 1080
 DB 1021 GCTACAGTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 1080
 OY 1081 GAAAGAACTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 1140
 DB 1081 GAAAGAACTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 1140
 OY 1141 GCTCAGAGAGAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 1200
 DB 1141 GCTCAGAGAGAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 1200
 OY 1201 ACAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 1260
 DB 1201 ACAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 1260
 OY 1261 ATTGAAAGAGAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 1320
 DB 1261 ATTGAAAGAGAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 1320
 OY 1321 CTTGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 1380
 DB 1321 CTTGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 1380
 OY 1381 GTAGTTATGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 1440
 DB 1381 GTAGTTATGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 1440
 OY 1441 GATGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 1500

DB 1441 GAATGGGTAGATATGTTACAGAGATATGATGACCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 1500
 OY 1501 CTTCAAAATGAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 1560
 DB 1501 CTTCAAAATGAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 1560
 OY 1561 AAACCTGAGC--ACCTACGACAGCCGACGCAATGACGAGATGATG 1605
 DB 1561 AAACCTGAGCAGCAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAG 1608

RESULT 7

ABN71527/c
 ID ABN71527 standard; DNA; 2155561 BP.

ABN71527;

02-JUL-2002 (first entry)

Streptococcus polynucleotide SEQ ID NO 10967.

Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;

group A streptococcus; Streptococcus pyogenes; antibacterial; gene;

antibacterial; infection; vaccine; meningitis; gene therapy; ds.

Streptococcus sp.

MO200234771-A2.

02-MAY-2002.

29-OCT-2001; 2001MO-GB04789.

27-OCT-2000; 2000GB-0026333.

24-NOV-2000; 2000GB-0028727.

07-MAR-2001; 2001GB-0005640.

(CHIR-) CHIRON SPA.

(GENO-) INST GENOMIC RES.

Tellord J, Masignani V, Margalit Ros Yi, Grandi G, Fraser C;

Tellord J;

WPI: 2002-352536/38.

Claim 8; Page 4196-4488; 4525pp; English.

The invention relates to a protein (ABP25413-ABP30895) from group B
 streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
 (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 the specification. The proteins have antibacterial and anti-inflammatory
 activity. (i), nucleic acids encoding (i), ABN6044-ABN71526 and
 antibodies that bind (i) are used in the manufacture of medicaments for
 the treatment or prevention of infection or disease caused by
 Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 Nucleic acids encoding (i) are used to detect Streptococcus in a
 biological sample. (i) is used to determine whether a compound binds to
 (i). A composition comprising (i) or a nucleic acid encoding (i), may be
 used as a vaccine or diagnostic composition. The disease caused by
 streptococcus that is prevented or treated may be meningitis. Nucleic
 acid encoding (i) may be used to recombinantly produce (i) and may be
 used in gene therapy. Antibodies to (i) are used for affinity
 chromatography, immunoassays, and distinguishing/identifying
 Streptococcus proteins.

Sequence 2155561 BP; 695741 A; 385320 C; 382938 G; 691542 T; 0 other;

Query Match

64.9%; Score 1062.4; DB 24; Length 2155561;

PT resistant bacterial infections -

XX Claim 16, Page 231, 380pp; English.

XX The present invention relates to nucleic acids (AAH90701-AAH90918)
XX encoding polypeptides (AAH01002-AAH01114), which are essential for the
XX viability of a bacterial cell wall. The acronym CFE stands for "Cef For
XX Expression", where Cef stands for "Conserved Essential Gene". The nucleic
XX acids are useful for detecting the presence of proteins essential for the
XX viability of a bacterial cell wall in samples such as cells, tissues,
XX biological fluids, blood, serum, nose, ear or throat swabs with ligands,
XX and for detecting corresponding target nucleic acid molecules with
XX complementary sequences. The nucleic acids are also useful for
XX determining whether a genomic nucleotide sequence of interest is
XX essential for viability of a bacterial cell or whether it resides within
XX an operon, by integrating an exogenous nucleotide sequence comprising a
XX portion of an open reading frame of the genomic sequence of interest
XX (comprising 200-500 base pairs) into the genomic sequence of interest
XX which confers a selectable phenotype to the cell, and determining cell
XX viability with a selection agent such as chloramphenicol. The nucleic
XX acids and proteins are also useful as vaccines and for treating bacterial
XX infections with gene therapy and antisense therapy. The nucleic acids
XX also enable identification of targets suitable for the treatment of
XX antibiotic resistant bacterial infections.

XX Sequence 1623 BP; 490 A; 325 C; 394 G; 414 T; 0 other;

Query Match 63.4%; Score 1039.2; DB 22; Length 1623;

Best Local Similarity 77.6%; Pred. No. 6,6e-262;

Matches 1257; Conservative 0; Mismatches 363; Indels 0; Gaps 0;

QY 1 ATGCCAAGAAGAAATCAAAATTTTCAGCAGATGCGCGCTGCGATGGTGGCGGAGTTGAT 60
DB 1 ATGCCAAGAAGAAATCAAAATTTTCAGATGCGCGCTGCGATGGTGGTGGTGGTGGT 60
QY 61 ATGTAGCAGATACCGTCAAAAGTAAAGCTTGGTCTTAAGGGCGCAATGTTGTTCTGAA 120
DB 61 ATTTCTTGACAGACCTGTAAAGTAACTTGGACCAAAAGTGGCAATGTTGTTCTGAA 120
QY 121 AAAGCTTTGGTCTGCGCTTAATTAATTAAGACGGGGTAAACATTTCTTAAAGATGAA 180
DB 121 AAAGCTTTGGTCTGCGCTTAATTAATTAAGACGGGGTAAACATTTCTTAAAGATGAA 180
QY 122 AATGATTCGTTTACCTTGAATTAATTAAGACGGGGTAAACATTTCTTAAAGATGAA 180
DB 122 AATGATTCGTTTACCTTGAATTAATTAAGACGGGGTAAACATTTCTTAAAGATGAA 180
QY 181 TTGAAAGATCAATTTGAAAGATGGAAGAAATTTGTTGTTGTTGTTGTTGTTGTTGTT 240
DB 181 TTGAAAGATCAATTTGAAAGATGGAAGAAATTTGTTGTTGTTGTTGTTGTTGTTGTT 240
QY 241 AATGATTCGTTTACCTTGAATTAATTAAGACGGGGTAAACATTTCTTAAAGATGAA 300
DB 241 AATGATTCGTTTACCTTGAATTAATTAAGACGGGGTAAACATTTCTTAAAGATGAA 300
QY 301 GAAGGCTAAAGAAATGTGACAGAGTGTCAATCAATGTTGTTGTTGTTGTTGTTGTTGTT 360
DB 301 GAAGGCTAAAGAAATGTGACAGAGTGTCAATCAATGTTGTTGTTGTTGTTGTTGTTGTT 360
QY 361 ACAGCAACAGCAACAGCTGTTGAAGCTTGAAGCAATGTTGTTGTTGTTGTTGTTGTTGTT 420
DB 361 ACAGCAACAGCAACAGCTGTTGAAGCTTGAAGCAATGTTGTTGTTGTTGTTGTTGTTGTT 420
QY 421 GAAGCTATTCGTTGAGAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 480
DB 421 GAAGCTATTCGTTGAGAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 480
QY 481 TCGAAGCTATTCGTTGAGAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 540
DB 481 TCGAAGCTATTCGTTGAGAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 540
QY 541 ATGGAACAGAACTGTAAGTGTGTAAGCATTAATTTGACCGTGTGTTACCTGTCTCAA 600
DB 541 ATGGAACAGAACTGTAAGTGTGTAAGCATTAATTTGACCGTGTGTTACCTGTCTCAA 600
QY 601 TACATGGTCACAGACATGAAGAAATGTTGTTGAGACCTGTAAAGCCATTTATGTTAATC 660
DB 601 TACATGGTCACAGACATGAAGAAATGTTGTTGAGACCTGTAAAGCCATTTATGTTAATC 660

DB 601 TACATGGTCACAGATAGCGAAAAAATGTCGCTGACCTTGAAAAATCCGTACATTTGATT 660
QY 661 ACGGATTAAGAAAGTGTCAAAACATCCCAAGACATTTGGCACTCTGAGAGATTTCTTAA 720
DB 661 ACGGATTAAGAAAGTGTCAAAACATCCCAAGACATTTGGCACTCTGAGAGATTTCTTAA 720
QY 721 ACCAAGCTGATTTCTGATTTATTTGAGATGATGATGATGATGATGATGATGATGATGAT 780
DB 721 ACCAAGCTGATTTCTGATTTATTTGAGATGATGATGATGATGATGATGATGATGATGAT 780
QY 781 GTCTTGAACAGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 840
DB 781 GTCTTGAACAGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 840
QY 841 GATGCTGTAAAGCTATTCGTTGAGACATTCGTTGTTGAGAGTGTGTTGATGATTTACA 900
DB 841 GATGCTGTAAAGCTATTCGTTGAGACATTCGTTGTTGAGAGTGTGTTGATGATTTACA 900
QY 901 GAGGATCTAGAGCTGTAATTAAGATCTACATGACAGCCCTTGAGAGAGCTGTAA 960
DB 901 GAGGATCTAGAGCTGTAATTAAGATCTACATGACAGCCCTTGAGAGAGCTGTAA 960
QY 961 ATTCAGCTGTAAAGATAGCAGATTAATTTGTTGAGGTTGAGAGTGTGTTGATGATTT 1020
DB 961 ATTCAGCTGTAAAGATAGCAGATTAATTTGTTGAGGTTGAGAGTGTGTTGATGATTT 1020
QY 1021 GCTAACGTTATGCTACGATTAATTCGATTAATTAAGCAACATTTGATGATTTGACCT 1080
DB 1021 GCTAACGTTATGCTACGATTAATTCGATTAATTAAGCAACATTTGATGATTTGACCT 1080
QY 1081 GAAAGCTCAAGAACTTTGGGAAATTTAGCTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1140
DB 1081 GAAAGCTCAAGAACTTTGGGAAATTTAGCTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1140
QY 1141 GCTCAACAGACAGCTTTAAAGAAATGAACTTCGATTTGAGATGCTTAAATGCT 1200
DB 1141 GCTCAACAGACAGCTTTAAAGAAATGAACTTCGATTTGAGATGCTTAAATGCT 1200
QY 1201 ACAGCTGCAAGCCGTTGAGAAAGTATCGTTGCTGTTGTTGTTGTTGTTGTTGTTGTT 1260
DB 1201 ACAGCTGCAAGCCGTTGAGAAAGTATCGTTGCTGTTGTTGTTGTTGTTGTTGTTGTT 1260
QY 1261 ATTGAAGAAAGTACAGCTCTTACCTGAGGCGGATGATGCTGATGATGATGATGATGAT 1320
DB 1261 ATTGAAGAAAGTACAGCTCTTACCTGAGGCGGATGATGCTGATGATGATGATGATGAT 1320
QY 1321 CTTCGTTGCTTGAAGAGCCCTGAGCTCAATGCTTAAATGCTGTTGTTGTTGTTGTT 1380
DB 1321 CTTCGTTGCTTGAAGAGCCCTGAGCTCAATGCTTAAATGCTGTTGTTGTTGTTGTT 1380
QY 1381 GTAGATATTGACAAAGTTGAAAAACAGCCCTGACAGAACAGATTTAATCTGCAAGCT 1440
DB 1381 GTAGATATTGACAAAGTTGAAAAACAGCCCTGACAGAACAGATTTAATCTGCAAGCT 1440
QY 1441 GAGTGGTTGATGATTAAGAGAGAAATGATGATGATGATGATGATGATGATGATGAT 1500
DB 1441 GAGTGGTTGATGATTAAGAGAGAAATGATGATGATGATGATGATGATGATGATGAT 1500
QY 1501 CTTCAAATGAGCTTGTAGCTAGTCTTATTTGAGACAGAAACAGATTTGTTGTTGTT 1560
DB 1501 CTTCAAATGAGCTTGTAGCTAGTCTTATTTGAGACAGAAACAGATTTGTTGTTGTT 1560
QY 1561 AAACCTGACAGCTACAGCAGCAGCAGCAATCCAGAGAGTTGATCCAGAAATGATG 1620
DB 1561 AAACCTGACAGCTACAGCAGCAGCAGCAATCCAGAGAGTTGATCCAGAAATGATG 1620

RESULT 9
AAF25036
ID AAF25036 standard; DNN: 1926 BP.
XX
XX AAF25036;
XX

DT 30-APR-2001 (first entry)
 XX Nucleotide sequence of Hsp65-E7 fusion protein.
 DE Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
 KM Lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
 KW E7 protein; ss.
 XX
 OS Synthetic.
 OS Streptococcus pneumoniae.
 OS Human papillomavirus.
 XX
 FH Location/Qualifiers
 FT 1..1926
 FT /tag- a
 FT /product- "Hsp65-E7 fusion protein"
 PN WO200104344-A2.
 XX
 PD 18-JAN-2001.
 XX
 PF 10-JUL-2000; 2000WO-US18828.
 XX
 PR 08-JUL-1999; 99US-0143757.
 XX
 PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
 XX
 PI Siegel M, Chu NR, Milzen LA;
 XX
 DR WPI: 2001-138361/14.
 DR P-PSDB; AAB31619.
 XX
 PT Screening for compounds that stimulate Th1-like responses in CD4+ T
 PT lymphocyte cells
 PS Example 15; Fig 15A-B; 88pp; English.
 CC The present sequence encodes a fusion protein comprising a
 CC Streptococcus pneumoniae heat shock protein (Hsp) 65 fused to a HPV16 E7
 CC protein. The fusion protein is used in the method of the invention. The
 CC specification describes a method of determining whether a compound
 CC stimulates a Th1-like response. Th1 cells are a subset of CD4+
 CC T lymphocyte cells. The method comprises contacting naive lymphocytes
 CC in vitro with a fusion protein comprising at least a fragment of Hsp,
 CC and then detecting the Th1-like response exhibited by the cell sample.
 CC The proteins which may be used in the method of the invention are Hsp65,
 CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify
 CC compounds that stimulate Th1-like responses in response to microbial
 CC pathogens.
 CC
 SQ Sequence 1926 BP: 585 A; 382 C; 464 G; 495 T; 0 other:
 Query Match 63.4%; Score 1038.4; DB 22; Length 1926;
 Best Local Similarity 77.5%; Pred. No. 1..1e-261;
 Matches 1258; Conservative 0; Mismatches 366; Indels 0; Gaps 0;

DB 241 AATGATATCGTGATGAGCACTACTGACAGATTGTTGACACAGCAATGTTCTT 300
 QY 301 GAAGCACTAAAAATGTCACACAGGTGCTAATGCTATGCTGAGGCAATGAA 360
 DB 301 GAAGCACTAAAAATGTCACACAGGTGCTAATGCTATGCTGAGGCAATGAA 360
 QY 361 ACAGCAAGCAACAGCTGTTGAGCCTTGAAGCCATTGCTCAACCTGATGCGAAG 420
 DB 361 ACAGCAAGTTGCCAGCAGTTGAGCTTTGAAAAAACAAGCATCCCTGTCCTCAAT 420
 QY 421 GAAGCTATGCTGAGTCCGTCAGTATCATCAGCTGCTGAAAAAGTGGAGATATATC 480
 DB 421 GAAGCTATGCTGAGTCCGTCAGTATCATCAGCTGCTGAAAAAGTGGAGATAT 480
 QY 481 TCAGAGCTATGAGAGGTGGAGGAGATGATTCATCCAGAAATGCTGAGGT 540
 DB 481 TCAGAGCTATGAGAGGTGGAGGAGATGATTCATCCAGAAATGCTGAGGT 540
 QY 541 ATGGAAGCAATGAAAAAGTTGGCAAAAGCGTGTATCATCATCAAGATCAGTGGT 540
 DB 541 ATGGAAGCAATGAAAAAGTTGGCAAAAGCGTGTATCATCATCAAGATCAGTGGT 540
 QY 601 TACATGCTCAGACACATGAAAAAATGTTGACAGCTTGAATATCTTAATC 660
 DB 601 TACATGCTCAGACATGAAAAAATGTTGACAGCTTGAATATCTTAATC 660
 QY 661 ACGATATAAAGTGTCAACATCCAGACATTTTGCACACTGAGAGAGTCTTAAT 720
 DB 661 ACGACAGAAAAATTTCCAAATATCCAGAAATCTTGCACTTTGAAAAAGATCTCA 720
 QY 721 ACCAAGCTCATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 780
 DB 721 ACCAAGCTCATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 780
 QY 781 GTCTGAAACAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 840
 DB 781 GTCTGAAACAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 840
 QY 841 GATGCTGTAACCTATGCTGTAAGCAATGCTATCTTGAAGCTGATGATGATGAT 900
 DB 841 GATGCTGTAACCTATGCTGTAAGCAATGCTATCTTGAAGCTGATGATGATGAT 900
 QY 901 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
 DB 901 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
 QY 961 ATTACAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
 DB 961 ATTACAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
 QY 1021 GCTAAGCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 DB 1021 GCTAAGCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 QY 1081 GAAAAAATGCAAGAAAGTGGGCAATATGCTGATGATGATGATGATGATGATGAT 1140
 DB 1081 GAAAAAATGCAAGAAAGTGGGCAATATGCTGATGATGATGATGATGATGATGAT 1140
 QY 1141 GCTCAAGCAAGCAAGCTTTAAGAAATGAAATGCTGATGATGATGATGATGATGAT 1200
 DB 1141 GCTCAAGCAAGCAAGCTTTAAGAAATGAAATGCTGATGATGATGATGATGATGAT 1200
 QY 1201 ACAGCTGACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
 DB 1201 ACAGCTGACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
 QY 1261 ATTGAAAAAGTGTGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1320
 DB 1261 ATTGAAAAAGTGTGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1320
 QY 1321 CTTGAGCTCTGAGAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1380
 DB 1321 CTTGAGCTCTGAGAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1380

Db 1321 CTCCTGCTTGGAGAACCTGTCGTAATTCGTCACATGAGATTTGAGAGTCT 1380
QY 1381 GTAGTTATGACAGTTGAAAAAGACCCCTGACGAGAACGATTTAATGTCACACAGT 1440
Db 1381 ATGTTATGATCGTTTGAATAATCTGAGCTGTGATGATTCACAGCAACAGTCCG 1440
QY 1441 GAGTGGCTGATGATTAATAACAGGATCATTTGACCTGTGCAAAAGTAACAGATCAGC 1500
Db 1441 GAGTGGCTGATGATTAATAACAGGATCATTTGACCTGTGCAAAAGTAACAGATCAGC 1500
QY 1501 CTTCAGAAATGACAGCTTCTGACCTAGTCTTATTTGACAGAGAGAGAGTGTGCTAT 1560
Db 1501 CTTCAGAAATGACAGCTTCTGACCTAGTCTTATTTGACAGAGAGAGAGTGTGCTAT 1560
QY 1561 AATCGTGAACAGCTACGCGGACGAGCAATGCGACAGATGATCCAGAAATGATG 1620
Db 1561 AATCGTGAACAGCTACGCGGACGAGCAATGCGACAGATGATCCAGAAATGATG 1620
QY 1621 GGTG 1624
Db 1621 GGAG 1624

RESULT 10

AAK86153
ID AAK86153 standard; DNA; 1654 BP.

AAK86153:

22-SEP-1999 (first entry)

DNA encoding a Streptococcus pneumoniae heat shock protein (Hsp)60-2.

Heat shock protein; Hsp60-2; Immune response; immunological carrier; cancer control; tumour; sarcoma; cancer; gene therapy; ss.

Streptococcus pneumoniae.

MO9935270-A1.

15-JUL-1999.

29-DEC-1998; 98MO-CA01203.

31-DEC-1997; 97US-0001737.

(STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

Mizzen L, Wisniewski J;

WPI: 1999-430397/36.

P-PDB: AAY23902.

New nucleic acid encoding heat shock protein-60 from Streptococcus, useful in vaccines, as carriers for other immunogens, as anticancer agents and for diagnosis

Claim 3; Fig 2A-B; 176p; English.

The present sequence encodes a heat shock protein, designated Hsp60-2. The protein, its fragments, variants and fusion proteins, are used to elicit or enhance an immune response against Streptococcus, and to elicit a similar response to a target antigen fused to the protein. Unlike other immunological carriers, Hsp60 proteins are not immunosuppressive so provide an increased response to any conjugated or fused antigen. Also, where used for cancer control, they lack the side effects associated with endotoxins. They can also be used to detect specific antibodies and in treatment or prevention of tumours (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or liver). The Hsp60 polynucleotide is used for recombinant production of the protein, as a source of primers and probes for detecting streptococcal in standard hybridization/amplification assays, and therapeutically in gene therapy vectors.

XX
SO Sequence 1654 BP; 500 A; 326 C; 401 G; 427 T; 0 other;
Query Match 63.4%; Score 1038; DB 20; Length 1654;
Best local similarity 77.5%; Pred. No. 1.4e+261;
Matches 1257; Conservative 0; Mismatches 363; Indels 0; Gaps 0;
QY 1 ATGGCAAAATCAATTTTACAGATGCGGCTGCTCCATGTCGCGGAGTGTAT 60
Db 15 ATGGCAAAATCAATTTTACAGATGCGGCTGCTCCATGTCGCGGAGTGTAT 74
QY 61 ATGTACAGATACCGTCAAAAGTAACGCTGTGCTTAAGGCGCAATGTTGTTGAA 120
Db 75 ATCTTGCAAGTACTGTTAAAGTAACCTTGGACCAAAAGTGCATATGTCCTTGAA 134
QY 121 AAAGCTTTGCTCTCCCTTAATTAATATGACGGGGTAACCATGCTAAAGATCGAA 180
Db 135 AAGTCATTCGCTTCAACCTTGATTAACCAATGCGGTGATGATGCAAAAGATTA 194
QY 181 TTAGAGATCATTTTGAAGACATGAGCAAAATGATGTCGTAAGGCTGCTAAAC 240
Db 195 TTAGAGATCATTTTGAAGACATGAGCAAAATGATGTCGTAAGGCTGCTAAAC 254
QY 241 AATGATATGCTGTGATGAGGAGCACTACTGCAAGTTTGTACAGACATGTCAT 300
Db 255 AATGATATGCTGTGATGAGGAGCACTACTGCAAGTTTGTACAGACATGTCAT 314
QY 301 GAAGACTAAATAATGACAGAGAGGCTGTAATGCAATTTGATTCCTGAGACATGAA 360
Db 315 GAAGACTAAATAATGACAGAGAGGCTGTAATGCAATTTGATTCCTGAGACATGAA 374
QY 361 ACACCAACAGCAACAGCTGTTGAAGCTTTGAAGCCATGCTCAACCTGATCTGCAAG 420
Db 375 ACACCAACAGCAACAGCTGTTGAAGCTTTGAAGCCATGCTCAACCTGATCTGCAAG 434
QY 421 GAGCTATTTGCTCAAGTGGCTGCAATCATCAGCTGTGAAGAAAGTTGGAGATATC 480
Db 435 GAGCTATTTGCTCAAGTGGCTGCAATCATCAGCTGTGTGAAGAAAGTTGGAGATATC 494
QY 481 TCAGAACATATGAGCGTGTGGCAACAGATGTGATTAATCATCGAAGATCTGAGT 540
Db 495 TCAGAACATATGAGCGTGTGGCAACAGATGTGATTAATCATCGAAGATCTGAGT 554
QY 541 ATGAAACAGACTGAAGTGGTGAAGCATGATTTGACCGGTTCACGCTCAA 600
Db 555 ATGAAACAGACTGAAGTGGTGAAGCATGATTTGACCGGTTCACGCTCAA 614
QY 601 TACATGTCAGACATGAAAAATGCTGACAGCTTGAAACCATTTATCTTAATC 660
Db 615 TACATGTCAGACATGAAAAATGCTGACAGCTTGAAACCATTTATCTTAATC 674
QY 661 ACGGATTAAGATGTCAAACATCCAGACATTTTGCACACTTGTGAGGAATCTTAA 720
Db 675 ACGGATTAAGATGTCAAACATCCAGACATTTTGCACACTTGTGAGGAATCTTAA 734
QY 721 ACGAAGCTCATTAATCATATGACAGATGATGATGATGAGACATCTCAACCTT 780
Db 735 ACGAAGCTCATTAATCATATGACAGATGATGATGATGAGACATCTCAACCTT 794
QY 791 GCTGTAAACAAATTCGTGATCTTCAATGCTGTTGCTGCAAGGCGAGAGATTTG 840
Db 795 GCTGTAAACAAATTCGTGATCTTCAATGCTGTTGCTGCAAGGCGAGAGATTTG 854
QY 841 GATCGCTGAAGATGCTGATGAAACATTTGCAATTTGACAGTGTGACATGATTA 900
Db 855 GATCGCTGAAGATGCTGATGAAACATTTGCAATTTGACAGTGTGACATGATTA 914
QY 901 GAGATCTGAGCTGATTAAGATTAAGATCTTAAGTCAAGACAGCTTGAAGCTTAAG 960
Db 915 GAGATCTGAGCTGATTAAGATTAAGATCTTAAGTCAAGACAGCTTGAAGCTTAAG 974
QY 961 ATTACAGTTAAAGATTAAGATTAAGTGAAGTTCAGGAGTTGATTAAGATTA 1020

Db 975 GTGACCGTGGACAAAGATAGCAGCGTATTGTAGAGGTGCGAGAAATCTGAAGCATT 1034
 Qy 1021 GCTAACGATATTCATGATTAATGCAATTAGAAACACACCTTCGATGGACGCT 1080
 Db 1035 TCTCACGCTGTCCGTTATCAATGCAATCGAACTCAACTTCGATTTGACCGT 1094
 Qy 1081 GAAAACCTAGACAGCGTTGGCGAAATAGTGGTGGTGTGCTATCAACAAAGAGA 1140
 Db 1095 GAAAATTTGCAAGACGCTTGGCCAAATGTCAGTGTGCTATCAATGCTGCGA 1134
 Qy 1141 GCTCCAGACAGCGCTTAAAGAAATGAATCGCTATGAGATGCTTAAATGCT 1200
 Db 1155 GCGCCAGCTAAACGATGATTAAGAAATGAATCGCTGAGAAAGAGCCCTCAACGCT 1214
 Qy 1201 ACAGCTGACCGCTTGAAGAAAGATGCTGCTGCTGCTGGAACAGCACTTATTGCGTT 1260
 Db 1215 ACCTGCTACGCTGTGAAGAGATGCTGCTGCTGCTGGAACAGCACTTATTGCGTT 1274
 Qy 1261 ATGAAAGATGACAGCTCTTGAGCTTGAGCGCATGCTACTGACGTAACATTTGTG 1320
 Db 1275 ATTCACAGCTGTGCTACCTTGAGATGAGAGATGAGCAAGAGGACGTAATTTGTT 1334
 Qy 1321 CTTCGCTCTGTAGAACGCTGACGTCMAATTCCTTAAATGCTGGGTGAGAGGCTCC 1380
 Db 1335 CTCCGCTCTGTAGAACGCTGCTGCTCAATTCCTCAACATGAGATTTGAGAGATCT 1394
 Qy 1381 GATCTTATGACAAATTTGAAAAACACCCCTGAGGAACAGATTTAATGCTGCAACAGT 1440
 Db 1395 ATCTTATGATGATGCTTTGAAAAATGCTGAGCTGTGATGATTTAACAGCAACAGTGC 1454
 Qy 1441 GAGGGGTGATGATGATTTAAAGAGATGATTCATCCCTGTAAAGTACAGATGACG 1500
 Db 1455 GAGGGGTGATGATGATTTAAAGAGATGATTCATCCCTGTAAAGTACAGATGACG 1514
 Qy 1501 CTTCAAATGACGCTTCTGAGTACGCTTATTTTGAACAAGAGAGTGTGCTAAT 1560
 Db 1515 CTACAAATGACGCTTCTGAGTACGCTTATTTTGAACAAGAGAGTGTGCTAAT 1574
 Qy 1561 AAACCTGACAGCTGACGCGCAGCAATGCGAGATGATGATCCAGATGATG 1620
 Db 1575 AAACCTGACAGCTGACGCGCAGCAATGCGAGATGATGATGATGATGATGATG 1634
 Qy 1621 GG 1622
 Db 1635 GG 1636
 RESULT 11
 AAH90906
 ID AAH90906 standard; DNA; 1647 BP.
 AC AAH90906;
 DT 02-OCT-2001 (first entry)
 DE 2CFE 104 coding sequence.
 KW Antibacterial; vaccine; gene therapy; bacterial cell wall viability;
 KW CFE; CEG; Conserved Essential Gene; bacterial infection;
 KW antisease therapy; antibiotic resistance; ds.
 OS Streptococcus pneumoniae.
 PN W0200149721-A2.
 PD 12-JUL-2001.
 PF 29-DEC-2000; 2000MO-US35604.
 PR 30-DEC-1999; 99US-0174089.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.

PI Dougherty TJ, Pucci MJ, Dougherty BA, Davison DB, Bruccoleri RE;
 PI Thannasi JA;
 DR WPI: 2001-496721/54.
 XX
 PT Nucleic acids encoding conserved essential genes involved in bacterial
 PT replication which are potential targets for the treatment of antibiotic
 XX resistant bacterial infections .
 PS
 Claim 30; Fig 118; 380bp; English.
 The present invention relates to nucleic acids (AAH90701-AAH90918)
 encoding polypeptides (AAH01002-AAH01114), which are essential for the
 viability of a bacterial cell wall. The acronym CFE stands for "Conserved
 Expression", where CEG stands for "Conserved Essential Gene". The nucleic
 acids are useful for detecting the presence of proteins essential for the
 viability of a bacterial cell wall in samples such as cells, tissues,
 biological fluids, blood, serum, nose, ear or throat swabs with ligands,
 and for detecting corresponding target nucleic acid molecules with
 complementary sequences. The nucleic acids are also useful for
 determining whether a genomic nucleotide sequence of interest is
 essential for viability of a bacterial cell or whether it resides within
 an operon, by integrating an exogenous nucleotide sequence comprising a
 portion of an open reading frame of the genomic sequence of interest
 (comprising 200-500 base pairs) into the genomic sequence of interest
 which confers a selectable phenotype to the cell, and determining cell
 viability with a selection agent such as chloramphenicol. The nucleic
 acids and proteins are also useful as vaccines and for treating bacterial
 infections with gene therapy and antisease therapy. The nucleic acids
 also enable identification of targets suitable for the treatment of
 antibiotic resistant bacterial infections.

Sequence 1647 BP; 494 A; 340 C; 397 G; 416 T; 0 other:
 Query Match 63.2%; Score 1036; DB 22; Length 1647;
 Best Local Similarity 77.5%; Pred. No. 4,66-261;
 Matches 1255; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

Qy 1 ATGGCAAAAGAAATCAATTTTCAAGAGATGCGCGTCTGCATGCTGGCGGAGTTGAT 60
 Db 1 ATGTCAAAAGAAATTAATTTTCAATGATGATGCTGCTGATGCTGCTGCTGAT 60
 Qy 61 ATGTAGAGATACGCTCAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 Db 61 ATCTTTCAGACAGCTGTTAAAGTACCTTGAGCAACCAAGAGTGCMAATGCTCTTGA 120
 Qy 121 AAAGCTTTGGTTCCTTAAATTAATTAATGACGGGGTACCAATTCCTTAAGATCGAA 180
 Db 121 AAGTCAATTCGCTTACCTTATTAATTAATGACGGGGTACCAATTCCTTAAGATCGAA 180
 Qy 181 TTGAGATCATTTTGAAGAAATGCGAGCAAAATGCTGCTGAAGTGGCTTTAAACC 240
 Db 181 TTGAGAGCAATTTGAAATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 Qy 241 AATGATATTCGCTGATGAGGAGTACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 Db 241 AATGATATTCGCTGATGAGGAGTACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 Qy 301 GAAGGATTAAGAAATGATGACAGCTGCTAATCCAAATGCTGCTGCTGCTGCTGCTGCT 360
 Db 301 GAAGGATTAAGAAATGATGACAGCTGCTAATCCAAATGCTGCTGCTGCTGCTGCTGCT 360
 Qy 361 ACAGCAACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 Db 361 ACAGCACTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 Qy 421 GAAGCTATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 Db 421 GAAGCTATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 Qy 481 TCAGAACTGATGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 Db 481 TCTGAAGCAATGSAAGAAAGTTGCAAGAGCGTGTCTATCAGCATGAAAGTACGCTGCT 540

RESULT 12
 AAH56860
 ID AAH56860 standard; DNA: 2107 BP.
 AC AAH56860;
 DT 06-SEP-2001 (first entry)
 DE Antibiotic resistant *S. pneumoniae* groE operon sequence SEQ ID NO:6.
 XX
 XX Antisense oligonucleotide: groE: groEL: groES: inhibitor: growth:
 KM microorganism: *Escherichia coli*: *Streptococcus pneumoniae*: diagnosis:
 KM *Streptococcus pyogenes*: *Staphylococcus aureus*: *Pseudomonas aeruginosa*.
 KM antibacterial: antiviral: antiproliferative: antisense therapy;
 KM microbial infection: ds.
 XX
 OS *Streptococcus pneumoniae*.
 XX
 FN WO200136625-A2.
 XX
 FN 25-MAY-2001.
 XX
 PD 20-NOV-2000: 2000MO-CA01347.
 XX
 XX 18-NOV-1999: 99US-0166249.
 PR
 PA (GENE-) GENESENSE TECHNOLOGIES INC.
 XX
 PI Wright JA, Young AH, Dugourd D;
 DR WPI: 2001-355633/37.
 XX
 PT Novel antisense compounds targeting nucleic acid encoding groEL or
 PT groES gene of microorganism, which hybridize with and inhibit
 PT expression of the genes, useful to inhibit growth of microorganism
 PT having the genes -
 XX
 XX Disclosure: Fig 6; 110pp; English.
 XX
 XX The present invention specifically claims AAH56368 to AAH56832 which are
 CC antisense oligonucleotides to nucleotide sequences encoding groE. More
 CC generally, antisense compounds (I) comprising antisense oligonucleotides
 CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat
 CC shock protein (HSP)60) (GL) and groES (HSP10) (GS) gene from a
 CC microorganism, where the antisense compound is complementary to GL or
 CC GS of a microorganism and specifically hybridizes with and inhibits the
 CC expression of GL or GS, is claimed. (I) have antibacterial, antiviral
 CC and antiproliferative activities, and can be used in antisense therapy
 CC and for inhibition of expression of groES or groEL. (I) are useful for
 CC inhibiting expression of GL or GS in cells or tissues *in vitro*. (I) are
 CC also useful for inhibiting the growth of a microorganism, or inhibiting
 CC the expression of GL or GS gene in a microorganism (a bacterial cell or
 CC a virus) having a GL or GS gene which involves administering (I) to the
 CC microorganism or to a cell infected with the microorganism. (I) are
 CC also useful for treating a mammalian pathological condition mediated by
 CC the microorganisms which involves identifying a eukaryotic organism
 CC having a pathological condition mediated by microorganisms having a GL
 CC or GS gene and administering (I) such that the growth of microorganism
 CC is inhibited. The antisense compounds are utilized for diagnostics, for
 CC therapeutics, prophylaxis and as research reagents and kits, e.g., to
 CC prevent or delay microbial infections in humans. They are also useful as
 CC molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56854
 CC represent PCR primers for groE sequences which are used in the
 CC amplification of the present invention. AAH56855 to AAH56870 represent
 CC groE nucleotide sequence given in the present invention.
 XX
 XX Sequence 2107 BP: 650 A: 400 C: 508 G: 549 T: 0 other;
 XX
 Query Match 63.2%; Score 1036; DB 22; Length 2107;
 Best Local Similarity 77.5%; Pval. NO. 5e-261;
 Matches 1255; Conservative 0; Mismatches 365; Indels 0; Gaps 0

OY 1 ATGCCAAGAAATCAAAATTTTCAGCAGATGCGCGTCTCCATGATGCGGAGTTGAT 60
 DB 485 ATGTCAAAAGAAATTAATTTTCATCAGATGCGGTTCAACATATGTCGCGTGCAT 544
 OY 61 ATGTACAGATATCGCTCAAGTAAGTACGCTGCTCAAGGCGCAATGTTGTTGAA 120
 DB 545 ATCCCTGACATATCTTAAGTAACTTGGACCAACAGTGGTGGTCTTGA 604
 OY 121 AAGCTTGTGCTCCCTTAATTAATTAATGCGGTTAACATTTGCTAAGATCGAA 180
 DB 605 AATTCATTTGCTCAACATATTAACAGTACGCTGATGCAATGCGCAAGAAATGGA 664
 OY 181 TTAAGAAATATTTGAAACATGGAACAAATGCTGTGTAAGTGGCTTTAAACC 240
 DB 665 TTAGAACCATTTGAAATATGGTGGCAAAATGATGATACGAAGTACGTTAAACC 724
 OY 241 AATGATATGCTGTGATGAGCACTACTGCAACATTTTGACACAGCATTTGAT 300
 DB 723 AATGATATGCTGTGATGAGCACTACTGCAACATTTTGACACAGCATTTGAT 300
 OY 301 GAAAGCACTAAATAATGTCAGCAGTGTCTAATCAATTTGATGCTGCGAGCATTTGA 360
 DB 785 GAAAGCACTAAATAATGTCAGCAGTGTCTAATCAATTTGATGCTGCGAGCATTTGA 360
 OY 361 ACAGCAACGCAACAGCTGTGTAAGCTTTGAAAGCCTTGCACAGCCTGATATGCGCAAG 420
 DB 845 ACAGCAACGCTGCGGCGAGCATTTGAAAGCCTTGCACAGCCTGATATGCGCAAG 420
 OY 421 GAACTATGCTGAGTGTGCTGAGATATCATCAGCTTGTGAAAGTGTGAGATATTC 480
 DB 905 GAACTATGCTGAGTGTGCTGAGATATCATCAGCTTGTGAAAGTGTGAGATATTC 480
 OY 481 TCAAGATATGAGACGCTGTGGCAACAGTGTGATATTCATGCAAGATCTGAGGT 540
 DB 965 TCAAGATATGAGACGCTGTGGCAACAGTGTGATATTCATGCAAGATCTGAGGT 540
 OY 541 ATGGAACAGAACTTGAAGTGTGTAAGCAATTTGACCGTGTGCTGCTCA 600
 DB 1025 ATGGAACAGAACTTGAAGTGTGTAAGCAATTTGACCGTGTGCTGCTCA 600
 OY 601 TACATGCTCAGACAGCAATGAAATAATGCTTGCAGACCTTGAAGCCATTTATCTATC 660
 DB 1085 TACATGCTCAGACAGCAATGAAATAATGCTTGCAGACCTTGAAGCCATTTATCTATC 660
 OY 661 ACAGATATAAAGTGTCAAAACATCCAGACATTTTCCGCACTTGTGAGAAATGCTTAA 720
 DB 1145 ACAGATATAAAGTGTCAAAACATCCAGACATTTTCCGCACTTGTGAGAAATGCTTAA 720
 OY 721 ACCAAGCTGCTACTATCATATATGCAAGATGATGATGATGATGATGATGATGATGAT 780
 DB 1205 ACCAAGCTGCTACTATCATATATGCAAGATGATGATGATGATGATGATGATGATGAT 780
 OY 781 GTCTTAACAGATTTGCTGCTCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 DB 1265 GTCTTAACAGATTTGCTGCTCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 OY 841 GATGCTGTAAGCTATGCTTAAGACATTTGCTATCTTACAGAGTGTGATGATGATGAT 900
 DB 1335 GATGCTGTAAGCTATGCTTAAGACATTTGCTATCTTACAGAGTGTGATGATGATGAT 900
 OY 901 GAGGATCTAGACCTTGAATTAAGATCTAATATACAGCCTTGGACAGGCTGCTAAG 960
 DB 1385 GAGGATCTAGACCTTGAATTAAGATCTAATATACAGCCTTGGACAGGCTGCTAAG 960
 OY 961 AATGAGTGTGTAAGATGACAGTATGCTGTAAGATGCTGTAAGATGCTGTAAGATGCT 1020
 DB 1445 AATGAGTGTGTAAGATGACAGTATGCTGTAAGATGCTGTAAGATGCTGTAAGATGCT 1020
 OY 1021 GCTTAACGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 DB 1505 GCTTAACGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 OY 1081 GAAAACTACAGAACTTTGGCGAAATGATGCTGTGCTGATGCTTATCAAAATGAGA 1140

DB 1565 GAAAACTACAGAACTTTGGCGAAATTTGTCAGGCTGTGAGCGGTATTAAGTGGCA 1624
 OY 1141 GCTCAGAGAGACAGCTTTAAAGAAATGAACTTCCATGAGATGCTTAAAGCT 1200
 DB 1625 GCGGCACTGAAATGAGTGTGAAAGAAATGAACTTCCATGAGATGCTTAAAGCT 1684
 OY 1201 ACAGTGCAGCGCTTGAAGAGATGATGCTGTGAGTGTGAGAGACACTTATTAAGCT 1260
 DB 1685 ACAGTGCAGCGCTTGAAGAGATGATGCTGTGAGTGTGAGAGACACTTATTAAGCT 1260
 OY 1261 ATGAAAGATGAGACCTTGTAGCTTGAAGGAGATGATGCTGTGAGTGTGAGAGAC 1320
 DB 1745 ATGAAAGATGAGACCTTGTAGCTTGAAGGAGATGATGCTGTGAGTGTGAGAGAC 1320
 OY 1321 CTTCGCTCTAGAGAGCGCTTGTAGCTTGAAGGAGATGATGCTGTGAGTGTGAGAG 1380
 DB 1805 CTTCGCTCTAGAGAGCGCTTGTAGCTTGAAGGAGATGATGCTGTGAGTGTGAGAG 1380
 OY 1381 GTATGATATGACAAAGTTGAAACAGCCTTGCAGACAGATTTAATGCTGCAACAGT 1440
 DB 1865 GTATGATATGACAAAGTTGAAACAGCCTTGCAGACAGATTTAATGCTGCAACAGT 1440
 OY 1441 GATGCTGCTGATATGATTAAGCAAGATATGACCTTGCAGACAGATTTAATGCTGCA 1500
 DB 1925 GATGCTGCTGATATGATTAAGCAAGATATGACCTTGCAGACAGATTTAATGCTGCA 1500
 OY 1501 CTTCAGATGACCTTGTAGCTGATGCTTATTTGACACAGAGAGTGTGAT 1560
 DB 1985 CTTCAGATGACCTTGTAGCTGATGCTTATTTGACACAGAGAGTGTGAT 1560
 OY 1561 AAACCTGACACCTTGCAGAGCGGCGAGCAATGCGAGTGTGATGATGATGATGATGAT 1620
 DB 2045 AAACCTGACACCTTGCAGAGCGGCGAGCAATGCGAGTGTGATGATGATGATGATGAT 1620

RESULT 13

ID AAVS2210
 ID AAVS2210 standard; DNA: 5365 bp.

AC ANVS2210;
 DT 23-OCT-1998 (first entry)
 DE Streptococcus pneumoniae genome fragment SEQ ID NO:77.
 XX Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
 KM computer; readable medium; vaccine; pharmaceutical composition; de.
 OS Streptococcus pneumoniae.
 PN W09818931-A2.
 PD 07-MAY-1998.
 PF 30-OCT-1997; 97MO-US19588.
 PR 31-OCT-1996; 96US-0029960.
 RA (HUMA-) HUMAN GENOME SCI INC.
 PI Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M;
 PT Kunsch CA, Rosen CA;
 DR WPI: 1998-272225/24.
 XX Computer-readable medium with recorded Streptococcus pneumoniae
 PT polynucleotide sequences - useful in diagnostic kits and assays; and
 PT pharmaceutical compositions and vaccines for Streptococcus
 XX pneumoniae
 PS Claim 1; Page 628-631; 1409pp; English.

SQ Sequence 5365 BP; 1654 A; 960 C; 1082 G; 1669 T; 0 other;

Matches 1254; Conservative 0; Mismatches 366; Indels 0; Gaps 0;

[illegible]

DE 5. pneumoniae groE operon nucleotide sequence SEQ ID NO:5.
 XX
 XX Antisense oligonucleotide: groE; groEL; groES; inhibitor: growth;
 KW microorganism: Escherichia coli; Streptococcus pneumoniae; diagnosis;
 KW Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa;
 KW antibacterial; antiviral; antiproliferative; antisense therapy;
 KM microbial infection; ds.
 XX
 XX Streptococcus pneumoniae.
 XX
 XX WO200136625-A2.
 XX
 XX 25-MAY-2001.
 XX
 XX 20-NOV-2000: 2000WO-CA01347.
 XX
 XX 18-NOV-1999: 99US-0166249.
 XX
 XX (GENE-) GENESENSE TECHNOLOGIES INC.
 XX
 XX Wright JA, Young AH, Dugourd D;
 XX
 XX WPI: 2001-355633/37.
 XX
 XX Novel antisense compounds targeting nucleic acid encoding groEL or
 PT groE gene of microorganism, which hybridize with and inhibit
 PT expression of the genes, useful to inhibit growth of microorganism
 PT having the genes -
 XX
 XX
 XX Disclosure: Fig 5; 110pp; English.
 XX
 XX The present invention specifically claims AAH56368 to AAH56832 which are
 CC antisense oligonucleotides to nucleotide sequences encoding groE. More
 CC generally, antisense compounds (1) comprising antisense oligonucleotides
 CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat
 CC shock protein (HSP60) (GL) and groES (HSP10) (GS) gene from a
 CC microorganism, where the antisense compound is complementary to GL or
 CC GS of a microorganism and specifically hybridizes with and inhibits the
 CC expression of GL or GS, is claimed. (1) have antibacterial, antiviral
 CC and antiproliferative activities, and can be used in antisense therapy
 CC and for inhibition of expression of groE or groEL. (1) are useful for
 CC inhibiting expression of GL or GS in cells or tissues in vitro. (1) are
 CC also useful for inhibiting the growth of a microorganism, or inhibiting
 CC the expression of GL or GS gene in a microorganism (a bacterial cell or
 CC a virus) having a GL or GS gene which involves administering to the
 CC microorganism or to a cell infected with the microorganism, (1). (1) are
 CC also useful for treating a mammalian pathological condition mediated by
 CC the microorganisms which involves identifying a eukaryotic organism
 CC having a pathological condition mediated by microorganisms having a GL
 CC or GS gene and administering (1) such that the growth of microorganism
 CC is inhibited. The antisense compounds are utilized for diagnostics,
 CC therapeutics, prophylaxis and as research reagents and kits, e.g., to
 CC prevent or delay microbial infections in humans. They are also useful as
 CC molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56854
 CC represent PCR primers for groE sequences which are used in the
 CC exemplification of the present invention. AAH56835 to AAH56870 represent
 CC groE nucleotide sequence given in the present invention.
 CC
 XX
 XX Sequence 2401 BP: 743 A; 459 C; 568 G; 631 T; 0 other;
 XX
 XX Query Match 62.9%; Score 1029.6; DB 22; Length 2401;
 XX Best Local Similarity 77.2%; Pred. No. 2,56-259;
 XX Matches 1251; Conservative 0; Mismatches 369; Indels 0; Gaps 0;

DB 739 AAGTATTCGCTTACCCCTTATGATACAGTACAGTGTGACATTCCTCAAGAAATGAA 798
 OY 181 TTGAAGATCATTTTGAAGAAATGAGGAGCAAAATGGTGTCTGAGTGGCTTTAAACC 240
 DB 799 TTGGAAGACATTTTGAAGAAATGAGGAGCAAAATGGTGTCTGAGTGGCTTTAAACC 858
 OY 241 AATGATATTCGCTTATGAGTACAGTACTGACATGAGTGTGACAGCAAGCCATGTCAT 300
 DB 859 AATGATATTCGCTTATGAGTACAGTACTGACATGAGTGTGACAGCAAGCCATGTCAT 918
 OY 301 GAGGACATAAAGAAATGAGTACAGTACTGACATGAGTGTGACAGCAAGCCATGTCAT 360
 DB 919 GAGGACATCAAAAGTACAGTACTGACATGAGTGTGACAGCAAGCCATGTCAT 978
 OY 361 ACAGCAAGTACAGTACTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 420
 DB 979 ACAGCAAGTACAGTACTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1038
 OY 421 GAGGACATCAAAAGTACAGTACTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 480
 DB 1039 GAGGACATCAAAAGTACAGTACTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1098
 OY 481 TTGAAGATCATTTTGAAGAAATGAGGAGCAAAATGGTGTCTGAGTGGCTTTAAACC 540
 DB 1099 TTGGAAGACATTTTGAAGAAATGAGGAGCAAAATGGTGTCTGAGTGGCTTTAAACC 1158
 OY 541 ATGGAACAGAACTTGAAGTGTGAGGAGCAATTTGACCGTGTGACCTGTGACAA 600
 DB 1159 ATGGAACAGAACTTGAAGTGTGAGGAGCAATTTGACCGTGTGACCTGTGACAA 1218
 OY 601 TACATGTGTCAGACATGAAATGAGTGTGAGGAGCAATTTGACCGTGTGACCTGTGACAA 660
 DB 1219 TACATGTGTCAGACATGAAATGAGTGTGAGGAGCAATTTGACCGTGTGACCTGTGACAA 1278
 OY 661 ACGATTAAGAAAGTGTCAACATGCAAGCAATTTGACCGTGTGACCTGTGACAA 720
 DB 1279 ACGATTAAGAAAGTGTCAACATGCAAGCAATTTGACCGTGTGACCTGTGACAA 1338
 OY 721 ACGATTAAGAAAGTGTCAACATGCAAGCAATTTGACCGTGTGACCTGTGACAA 780
 DB 1339 ACGATTAAGAAAGTGTCAACATGCAAGCAATTTGACCGTGTGACCTGTGACAA 1398
 OY 781 GCTTGAAGAAAGTGTCAACATGCAAGCAATTTGACCGTGTGACCTGTGACAA 840
 DB 1399 GCTTGAAGAAAGTGTCAACATGCAAGCAATTTGACCGTGTGACCTGTGACAA 1458
 OY 841 GATGCTGAAGAAAGTGTCAACATGCAAGCAATTTGACCGTGTGACCTGTGACAA 900
 DB 1459 GATGCTGAAGAAAGTGTCAACATGCAAGCAATTTGACCGTGTGACCTGTGACAA 1518
 OY 901 GAGGATCTAGACATGATTAAGATGCTACATGAGTGTGACCGTGTGACCGTGTGAC 960
 DB 1519 GAGGATCTAGACATGATTAAGATGCTACATGAGTGTGACCGTGTGACCGTGTGAC 1578
 OY 961 ATTACAGTGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 DB 1579 GTGACCGTGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1638
 OY 1021 GCTAACCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 DB 1639 TCTACCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1698
 OY 1081 GAAAGATCAAGAAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1140
 DB 1699 GAAAGATCAAGAAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1758
 OY 1141 GCTCAAGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1200
 DB 1759 GCTCAAGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1818
 OY 1201 ACAGTGTGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1260

Db 1819 ACTGCTGACGCTGTTGAGAAAGATATTTGTCAGTGTGTGACACAGCTTGTCCAATGTG 1878
Qy 1261 ATTGAAAAAGTAGCAGCTCTGAGCTTGTAGGCGCATGATGCTAGTACGATTAACATGTG 1320
Db 1879 ATTCCAGCTGAAAGCTTACCTTGAATGACAGAGATGAAGAACACAGAGCTAATGTGTT 1938
Qy 1321 CTTCGCTCTAGAAAGAGCTGTACGTAATATGCTTAATGCTGGGACCAAGCTCC 1380
Db 1939 CTCCTGCTTGGAAAGACCGCTTGCAATATGCTCAACATGACAGATTTGAAGATCT 1998
Qy 1381 GTAGTTATTTGACAAAGTGAAGAACAGCCGACGAAAGAGATTTAATGCTCAACAGCT 1440
Db 1999 ATGCTTATGATGCTTTGAAAAATGCTGACCTGATGATGATTTAAGCAGCAACGTGCG 2058
Qy 1441 GAGTGGTGTATATGATTAAGAAAGAGATTTGACCTGCTCAAGTAAAGATCAGCG 1500
Db 2059 GATGGCTTAACATGATTAAGAGATGATGATGATGATTAAGAGTGAAGTGTGACGCC 2118
Qy 1501 CTTCAAATGACGCTTCTGTAGCTAGCTTATTTGACACAGAGAGATTTGCTTAT 1560
Db 2119 CTACAAATGACGATCTGTAGCTTATTTGACACAGAGAGATTTGCTTAT 2178
Qy 1561 AATCTGAACGACCTAGCGACCGCCAGCAATGCGACGATGATGATCAGAGATGATG 1620
Db 2179 AATCGAAGACGATGACCGCCAGCTCAGCAATGATGATGATGATGATGATGATGATG 2238

RESULT 15

ABA90521 ABA90521 standard; DNA; 2365589 BP.

XX ABA90521;

XX 16-MAY-2002 (first entry)

XX Genomic sequence of *Lactococcus lactis* IL1403.

XX Biotynthesis; biodegradation; lactic bacterium; yogurt; cheese; ds.

XX *Lactococcus lactis* IL1403.

XX FR2807446-A1.

XX 12-OCT-2001.

XX 11-APR-2000; 2000FR-0004630.

XX 11-APR-2000; 2000FR-0004630.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

XX Bolotline A, Sorokline A, Renault P, Ehrlich SD;

XX WPI; 2002-043418/06.

XX New nucleotide sequence useful in the identification of *Lactococcus*XX *lactis* and related species -

XX Claim 1; SEQ ID 1; 2504bp; French.

XX The present invention is related to a *Lactococcus lactis* nucleotide
XX sequence (ABA90521) and related proteins (AB553300-AB55621). The
XX nucleic acid sequence is useful in the detection and/or amplification of
XX related species. The proteins of the invention are useful for the
XX biosynthesis or biodegradation of a composition of interest. The
XX invention helps research in lactic bacteria, particularly useful in the
XX production of yogurt and cheese.

XX Note: The sequence data for this patent is based on equivalent patent
XX WO2001/77334 (published 18-OCT-2001) which is available in electronic
XX format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 2365589 BP; 765914 A; 415261 C; 420487 G; 763927 T; 0 other;

Query Match 58.38; Score 954.2; DB 24; Length 2365589;
Best Local Similarity 75.28; Pred. No. 2,2e-238;
Matches 1190; Conservative 0; Mismatches 393; Indels 0; Gaps 0;

Qy 1 ATGCAAAAGCAATCAATTTTCAGCAGATGCGGCTGCTGCGGAGGAGTAT 60
Db 398897 ATGCAAAAGCAATCAATTTTCAGCAGATGCGGAGGAGTAT 60
Qy 61 ATGTACAGATACCGCTCAAGTAAGTACGCTGCTTAAAGGAGGAGTAT 120
Db 398957 ATGTACAGATACCGCTCAAGTAAGTACGCTGCTTAAAGGAGGAGTAT 120
Qy 121 AAACCTTTGCTTCCCTTAATTAATGAGGAGGAGTATGCTTAAAGGAGTAT 180
Db 399017 AAACCTTTGCTTCCCTTAATTAATGAGGAGGAGTATGCTTAAAGGAGTAT 180
Qy 181 TTAGAAATCATTTTGAAGAAATGAGAGCAAAATGCTGCAAGCTTCTTAAAC 240
Db 399077 TTAGAAATCATTTTGAAGAAATGAGAGCAAAATGCTGCAAGCTTCTTAAAC 240
Qy 241 AATGATATGCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
Db 399137 AATGATATGCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
Qy 301 GAAAGACTTAAATATGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Db 399197 GAAAGACTTAAATATGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Qy 361 ACAGCAAGCAGCAGAGCTGTTGACCTTGAAGCCATGCTCAACCTGATCTGCAAG 420
Db 399257 ACAGCAAGCAGCAGAGCTGTTGACCTTGAAGCCATGCTCAACCTGATCTGCAAG 420
Qy 421 GAAAGCTATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Db 399317 GAAAGCTATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Qy 481 TCAGAACTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Db 399377 TCAGAACTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Qy 541 ATGCAAGCAAGCAGCAGAGCTGTTGACCTTGAAGCCATGCTCAACCTGATCTGCAAG 600
Db 399437 ATGCAAGCAAGCAGCAGAGCTGTTGACCTTGAAGCCATGCTCAACCTGATCTGCAAG 600
Qy 601 TACATGCTCAAGCAGCAGATGAAAAATGCTGCAAGCTTGAAGCCATGCTTATC 660
Db 399497 TACATGCTCAAGCAGCAGATGAAAAATGCTGCAAGCTTGAAGCCATGCTTATC 660
Qy 661 ACGGATAAAAAGTGTCAAAACATCCAGACATTTGCCATCTGAGAGATCTTAA 720
Db 399557 ACGGATAAAAAGTGTCAAAACATCCAGACATTTGCCATCTGAGAGATCTTAA 720
Qy 721 ACCAAGCTCCATTAATGATTTGAGATGATGATGATGATGATGATGATGATGATGAT 780
Db 399617 ACCAAGCTCCATTAATGATTTGAGATGATGATGATGATGATGATGATGATGATGAT 780
Qy 781 GTCTTGAACAGATGCTGCTGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 399677 GTCTTGAACAGATGCTGCTGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Qy 841 GATCGCTGAAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 399737 GATCGCTGAAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Qy 901 GAGGATCTGAGCTTCAATTAAGATGCTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
Db 399797 GAGGATCTGAGCTTCAATTAAGATGCTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
Qy 961 ATTCAGTTGATTAAGATGAGCAGTATGTTGAGAGGTTGAGAGGTTGAGAGGTTAT 1020
Db 399857 ATTCAGTTGATTAAGATGAGCAGTATGTTGAGAGGTTGAGAGGTTGAGAGGTTAT 1020

